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Supplement of

Soil bacterial community and functional shifts in response to altered snowpack in moist acidic tundra of northern Alaska

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Supplemental Information

Table S1 - List of targeted KEGG ortholog enzymes used in the PiCRUST analyses. For more information see materials and methods in main text.

Functional role	Enzyme name	EC number	KEGG orthology number
PRESENT IN SAMPLES			
Arabinoside degradation	arabinogalactan endo-beta-1,4-galactanase	3.2.1.89	K01224
	arabinan endo-1,5-alpha-L-arabinanase	3.2.1.99	K06113
Cellulose degradation	cellulase	3.2.1.4	K01179
	beta-glucosidase	3.2.1.21	K01188, K05349, K05350
	cellulose 1,4-beta-cellobiosidase (CBH)	3.2.1.91	K01225
Chitin degradation	chitinase (NAG)	3.2.1.14	K01183
	bifunctional chitinase/lysozyme	3.2.1.14 & 3.2.1.17	K13381
Nitrogen mobilization	leucyl aminopeptidase (LAP)	3.4.11.1	K01255
	urease	3.5.1.5	K01427, K01428, K01429, K01430, K14048
Lignin degradation	tyrosinase (phenol oxidase)	1.14.18.1	K00505
Pectin degradation	polygalacturonase	3.2.1.15	K01184
	alpha-L-rhamnosidase	3.2.1.40	K05989
Phosphate mobilization	alkaline phosphatase (AP)	3.1.3.1	K01077, K01113
	acid phosphatase (AP)	3.1.3.2	K01078, K01093, K09474, K03788, K14379
Superoxides	superoxide dismutase	1.15.1.1	K00518, K04564, K04565
	superoxide reductase	1.15.1.2	K05919
Xylan degradation	xylan 1,4-beta-xylosidase	3.2.1.37	K01198
NOT FOUND IN ANY SAMPLES			
	polyphenol oxidase	1.10.3.1	K00422

peroxidase	1.11.1.7	K00430
fructan beta-fructosidase	3.2.1.80	K03332
laccase (oxidoreductase)	1.10.3.2	K05909
eosinophil peroxidase	1.11.1.7	K10788
cytosol aminopeptidase	3.4.11.1 & 3.4.11.5	K11142
peroxiredoxin 6, 1-Cys peroxiredoxin	1.11.1.7, 1.11.1.15, & 3.1.1.-	K11188
lactoperoxidase	1.11.1.7	K12550
low molecular weight phosphotyrosine protein phosphatase	3.1.3.2 3.1.3.48	K14394
lysophosphatidic acid phosphatase type 6	3.1.3.2	K14395
acid phosphatase	3.1.3.2	K14410
beta-D-xylosidase 4	3.2.1.37	K15920

Figures S1-to-S6. Linear fit regressions of bacterial phyla abundance with respect to soil properties such as soil carbon-to-nitrogen ratio (C/N), soil carbon mass concentration (%C), soil nitrogen mass concentration (%N), and soil pH across all snow treatment sites and all soil depths. The bacterial relative abundance is ordered from most abundant phylum (Fig. S1) to least abundant (Fig S6). See table S2 for statistics and significance.

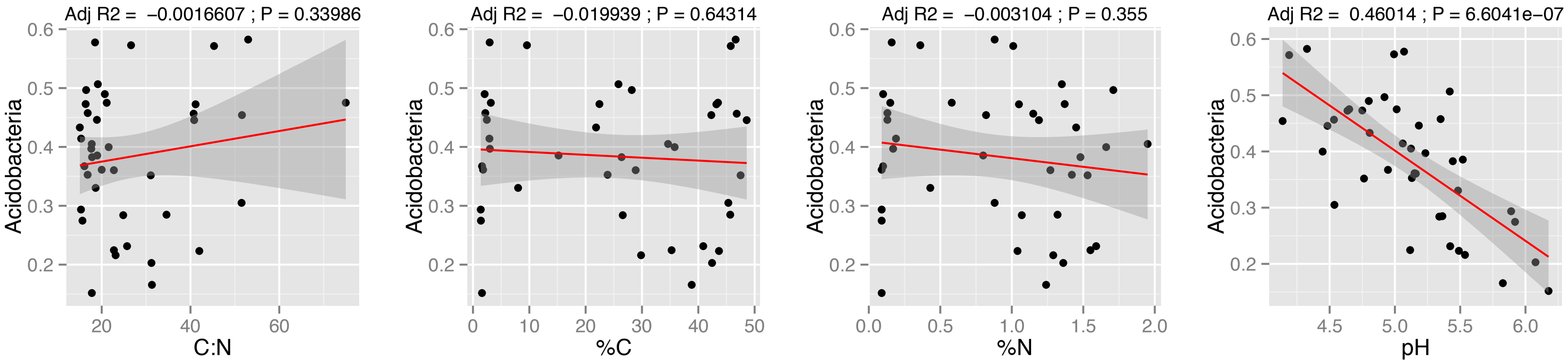

Fig. S1 – Linear relationships between Acidobacteria relative abundance and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

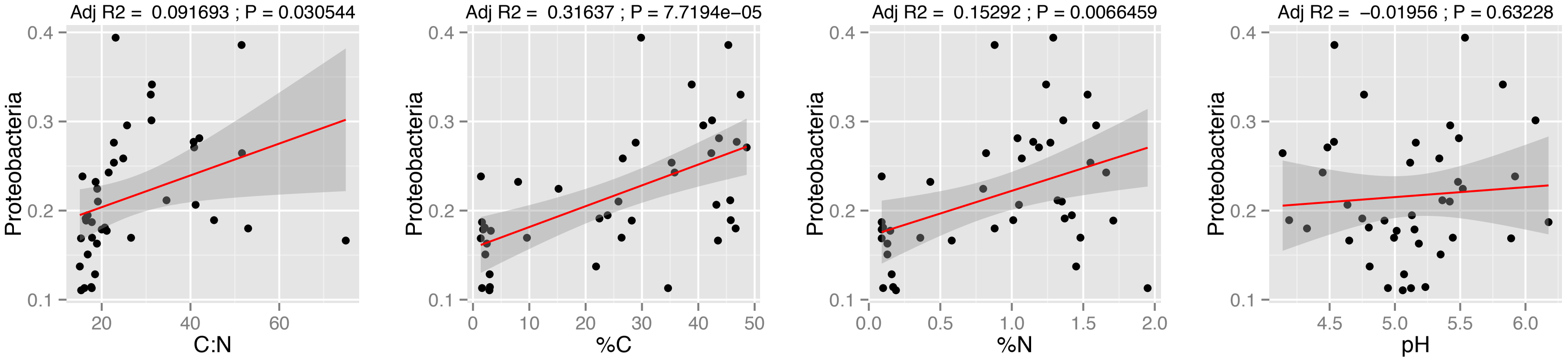

Fig. S2 – Linear relationships between Proteobacteria relative abundance and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

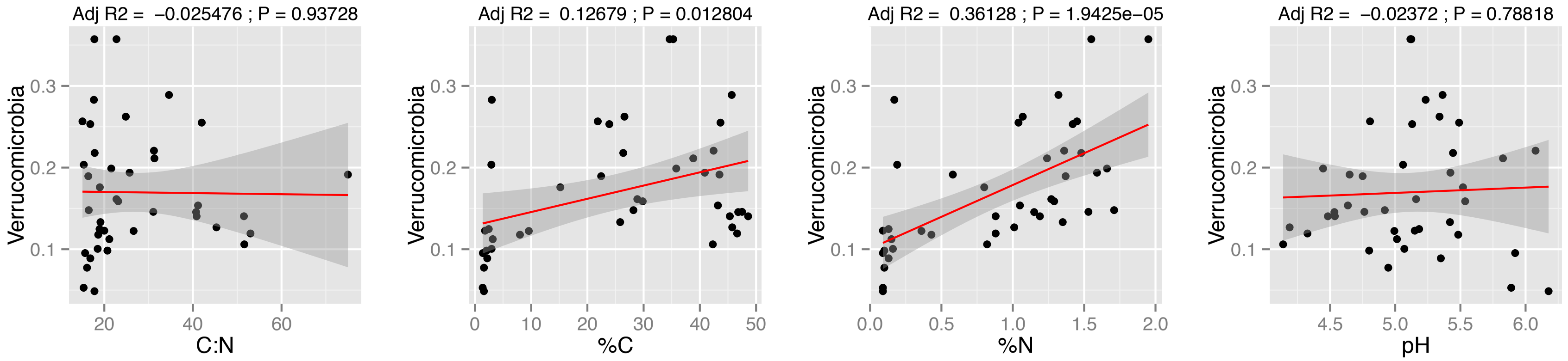

Fig. S3 – Linear relationships between Verrucomicrobia relative abundance and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

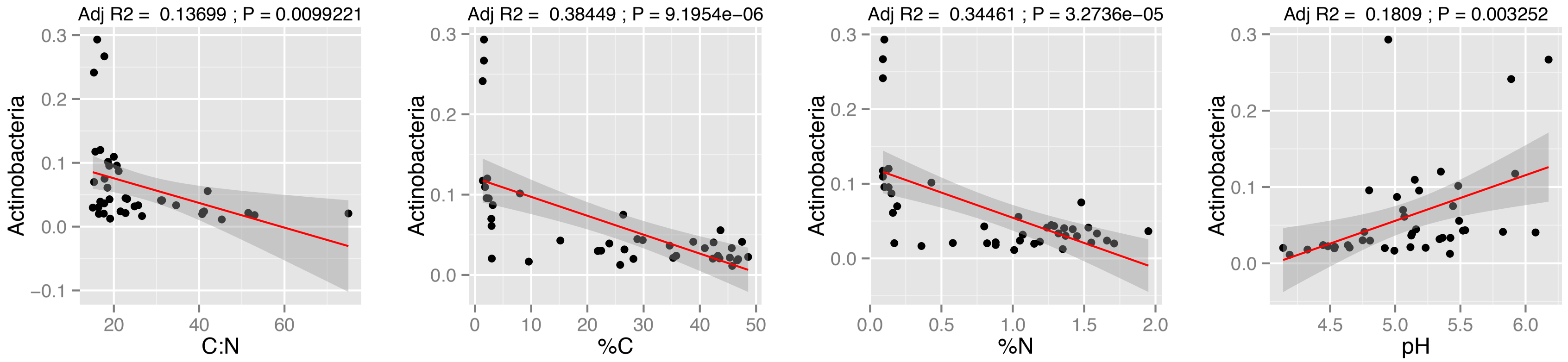

Fig. S4 – Linear relationships between Actinobacteria relative abundance and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

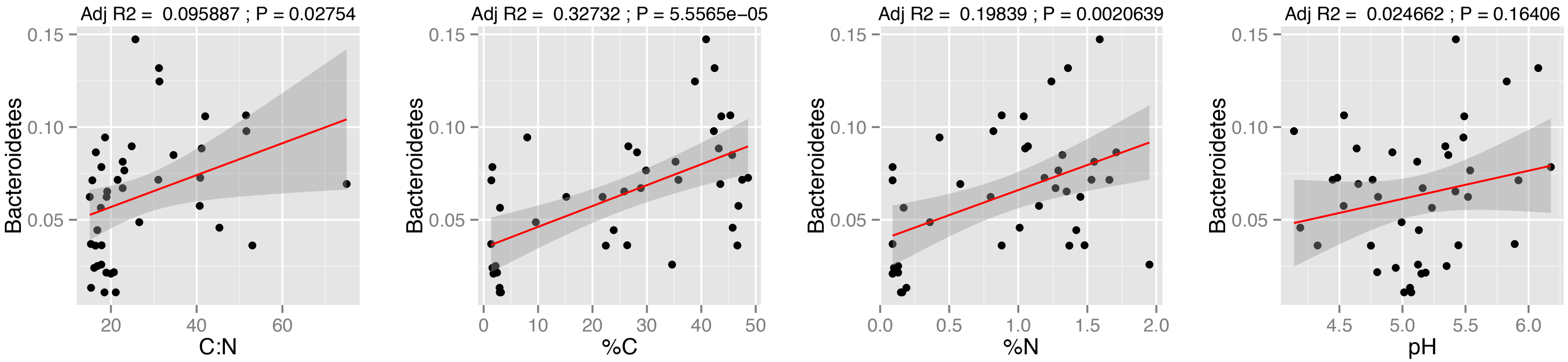

Fig. S5 – Linear relationships between Bacteroidetes relative abundance and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

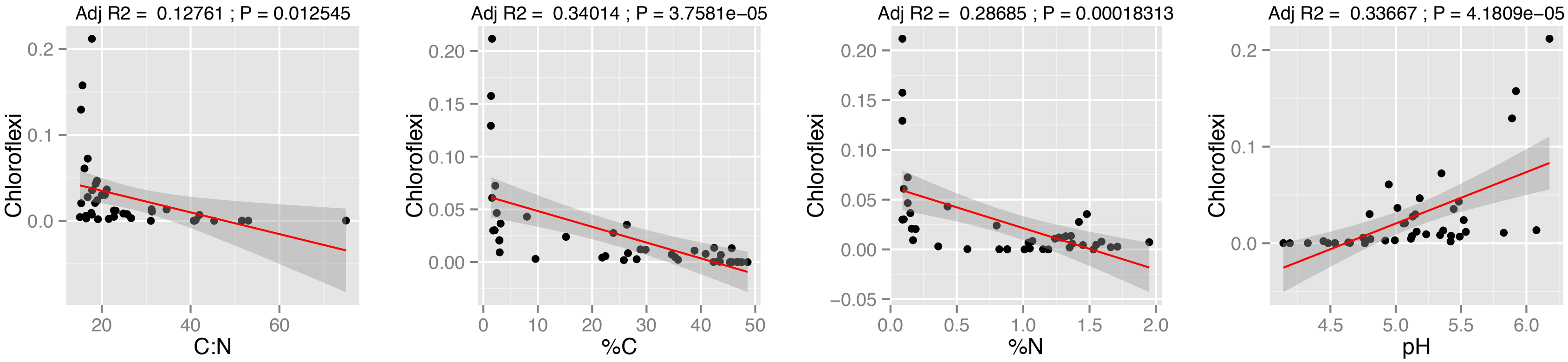

Fig. S6 – Linear relationships between Chloroflexi relative abundance and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

Figures S7-to-S15. Linear fit regressions of relative gene copy abundance with respect to soil properties such as soil carbon-to-nitrogen ratio (C/N), soil carbon mass concentration (%C), soil nitrogen mass concentration (%N), and soil pH across all snow treatment sites and all soil depths. Enzymes were grouped by their general activities as explained in main text and they are shown on the Y-axis of the figures. See table S2 for statistics and significance.

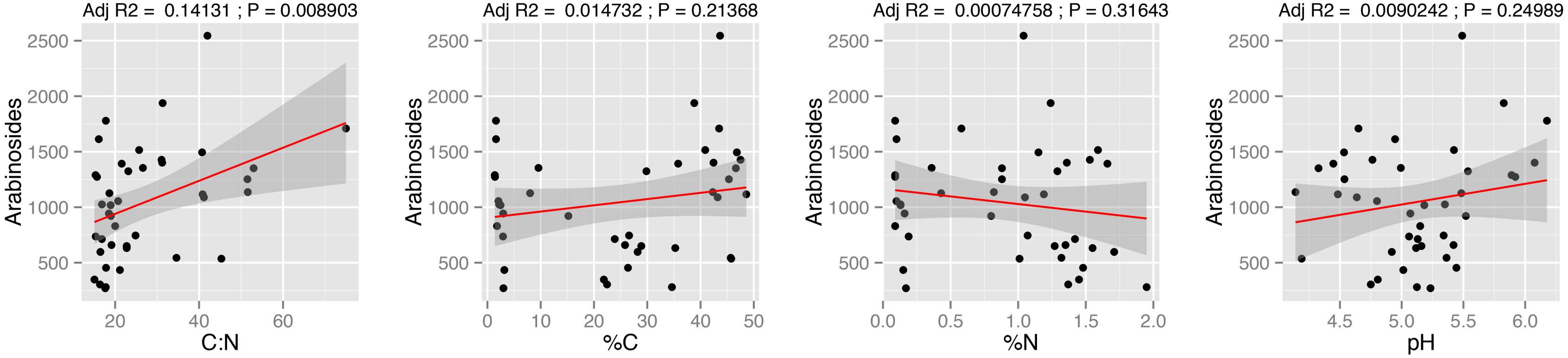

Fig. S7 – Linear relationships between the relative abundance of genes required for arabinoside degradation and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

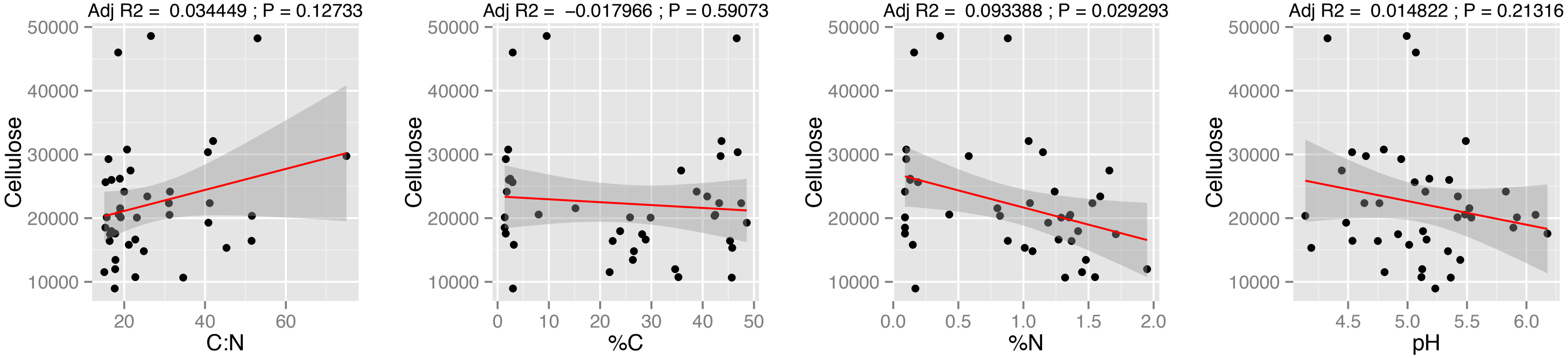

Fig. S8 – Linear relationships between the relative abundance of genes required for cellulose degradation and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

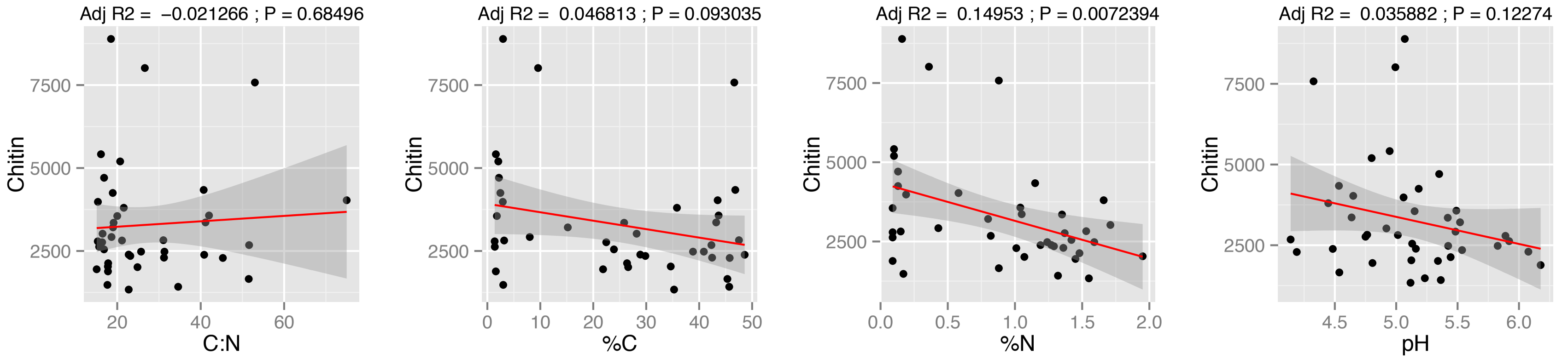

Fig. S9 – Linear relationships between the relative abundance of genes required for chitin degradation and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

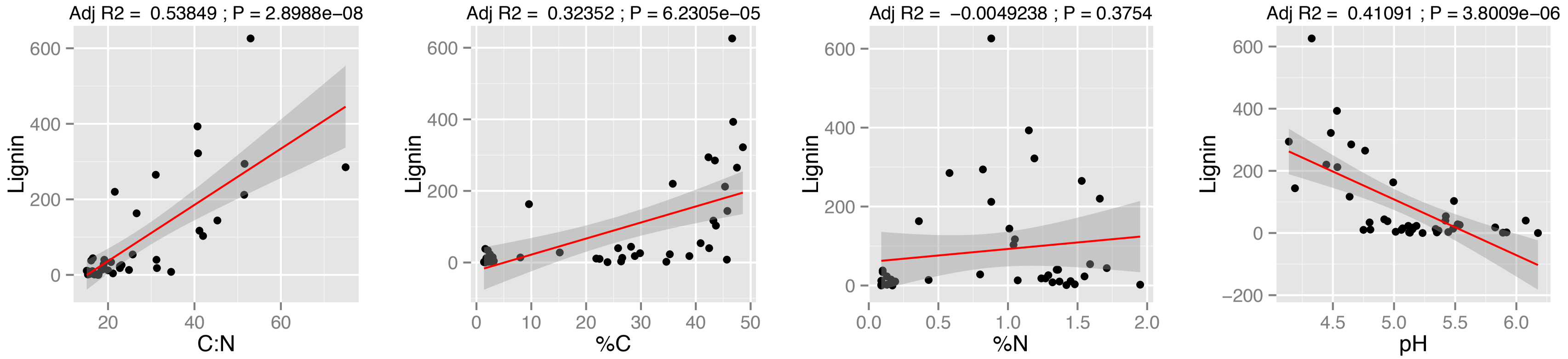

Fig. S10 – Linear relationships between the relative abundance of genes required for lignin degradation and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

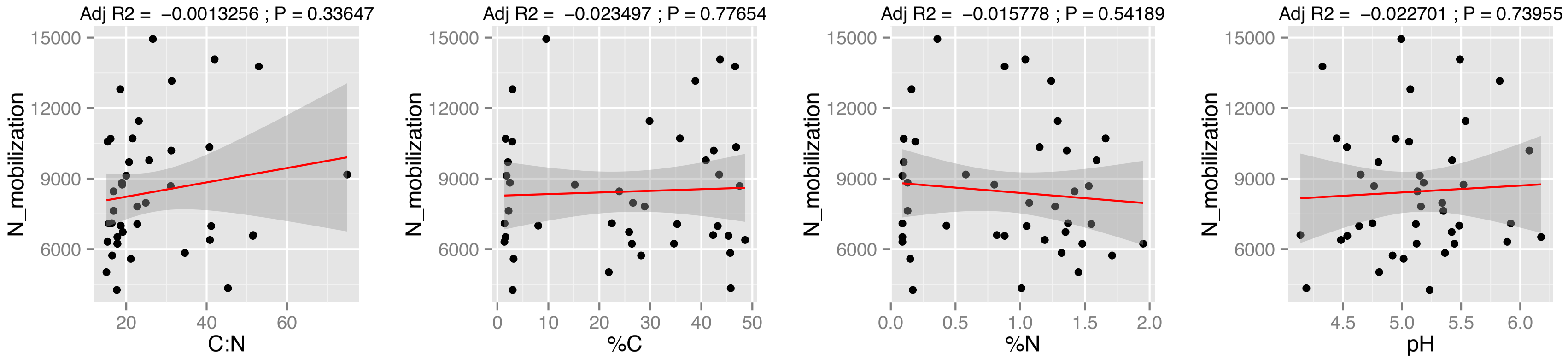

Fig. S11 – Linear relationships between the relative abundance of genes required for N mobilization and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

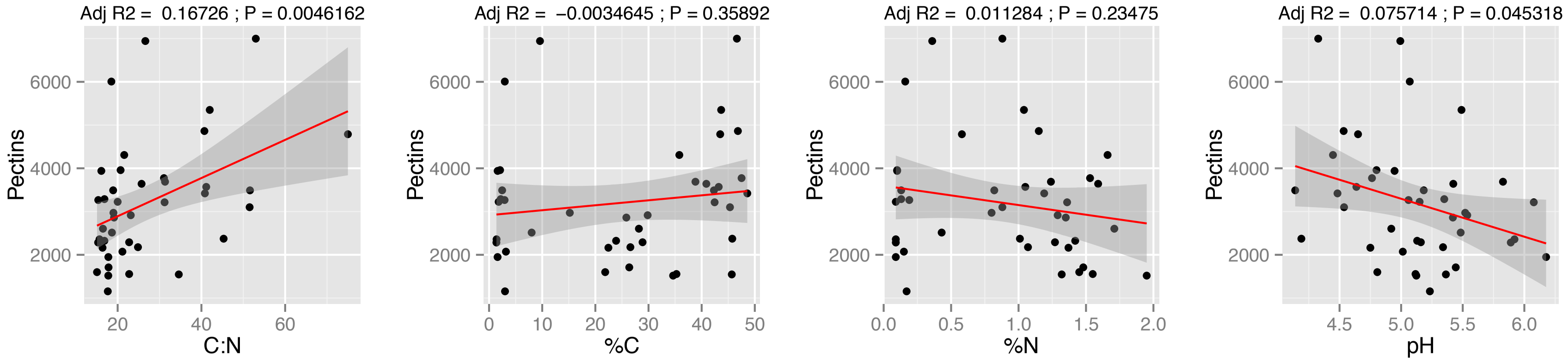

Fig. S12 – Linear relationships between the relative abundance of genes required for pectin degradation and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

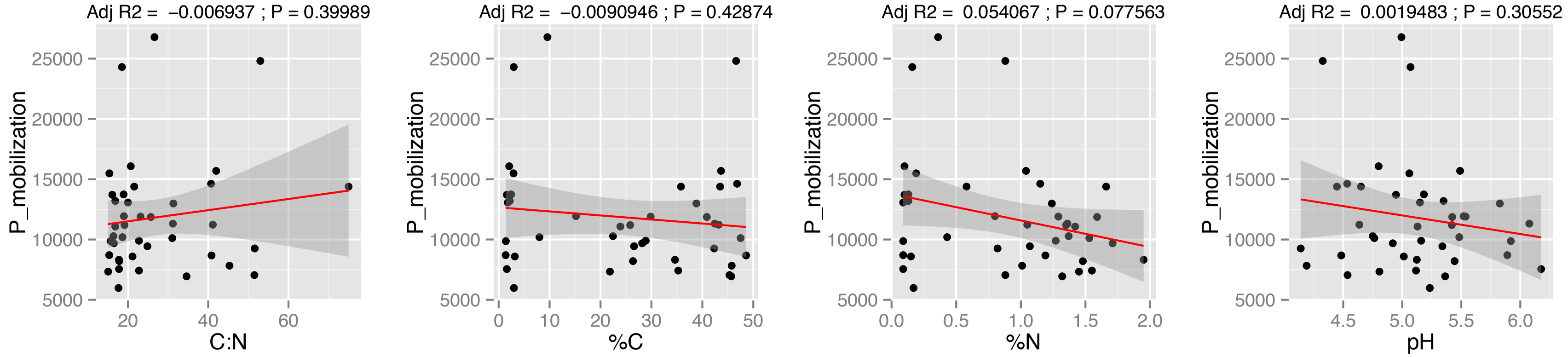

Fig. S13 – Linear relationships between the relative abundance of genes required for P mobilization and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

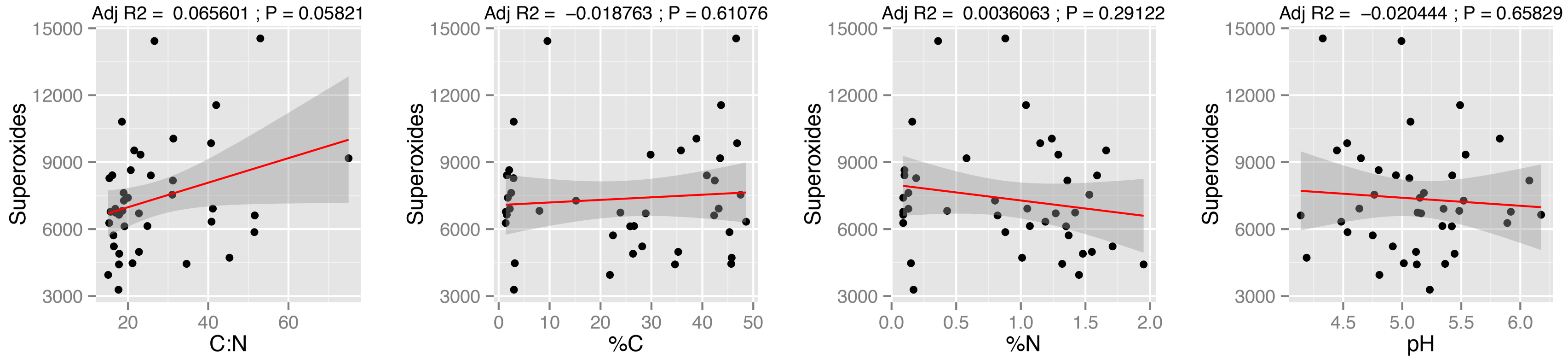

Fig. S14 – Linear relationships between the relative abundance of genes required for superoxide regulation and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

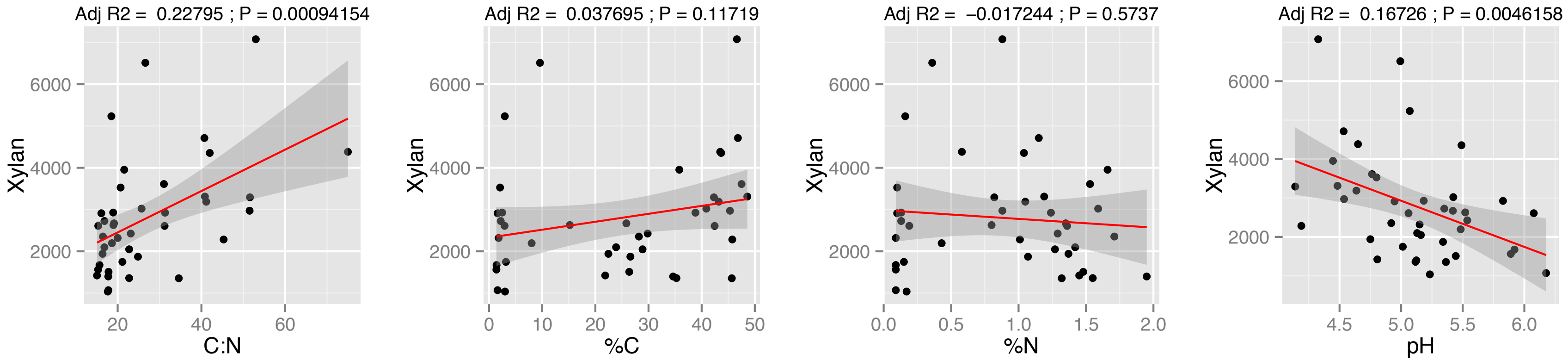

Fig. S15 – Linear relationships between the relative abundance of genes required for xylan degradation and soil C:N, C and N concentrations, and pH from all 41 samples. Shaded areas indicate 95% confidence intervals.

Table S2 – Effects of soil depth characteristics (Organic, Transition, Mineral) on soil chemistry, bacterial phylum relative abundance, and relative abundance of genes organized by functional groups, as determined by the Kruskal-Wallis test. Degrees of freedom = 2 for all analyses. * = $p<0.05$, ** = $p<0.01$, *** = $p<0.001$

	H-statistic	p-value	Soil layer w/ higher value (Org vs Min)
Soil Chemistry			
%C	32.32	9.57×10^{-8} ***	Organic
%N	26.53	1.74×10^{-6} ***	Organic
C:N	21.70	1.94×10^{-5} ***	Organic
pH	6.81	0.03 *	Mineral
Bacterial phylum abundance			
Acidobacteria	0.05	0.98	NA
Proteobacteria	14.78	6.17×10^{-4} ***	Organic
Verrucomicrobia	14.93	5.73×10^{-4} ***	Organic
Actinobacteria	20.16	4.12×10^{-5} ***	Mineral
Bacteroidetes	13.08	1.45×10^{-3} **	Organic
Chloroflexi	24.80	4.13×10^{-6} ***	Mineral
Enzyme gene abundance			
Lignin	20.17	4.17×10^{-5} ***	Organic
Chitin	3.00	0.22	NA
Cellulose	8.36	0.02 *	Organic
Pectin	17.25	1.80×10^{-4} ***	Organic
Xylan	15.79	3.72×10^{-4} ***	Organic
Arabinoside	13.62	1.10×10^{-3} **	Organic
N mobilization	11.67	2.92×10^{-3} **	Organic
P mobilization	3.30	0.19	NA
Superoxide	29.61	3.72×10^{-7} ***	Organic

Table S3 – Statistical analyses of alpha diversity using non-parametric two-sample t-tests with 999 Monte Carlo permutations. Pairwise comparisons of Shannon diversity metrics from each sample were made between each soil layer (Organic, Transition, Mineral) and each snow accumulation treatment (Control, Deep, Intermediate, Low).
* = $p<0.05$, ** = $p<0.01$, *** = $p<0.001$.

Two-sample t-tests		
Soil layers	t- statistic	p-value
Organic / Mineral	5.58	0.003 **
Trans / Organic	-0.26	1
Trans / Mineral	5.22	0.003**
Treatment		
Cont / Deep	0.30	1
Cont/ Int	-0.49	1
Cont / Low	1.70	0.6
Deep / Int	-4.0 x 10^{-4}	1
Deep / Low	-.30	1
Int / Low	0.51	1

Figures S16-S20. Heatmaps showing the relative raw abundance of operational taxonomic units (OTU) at different taxonomic levels (phyla, class, family, individual OTU) for each of the snow treatments: control (CTL), 100% more snow accumulation (DEEP), 50% more snow (INT), and 25% less snow than control (LOW).

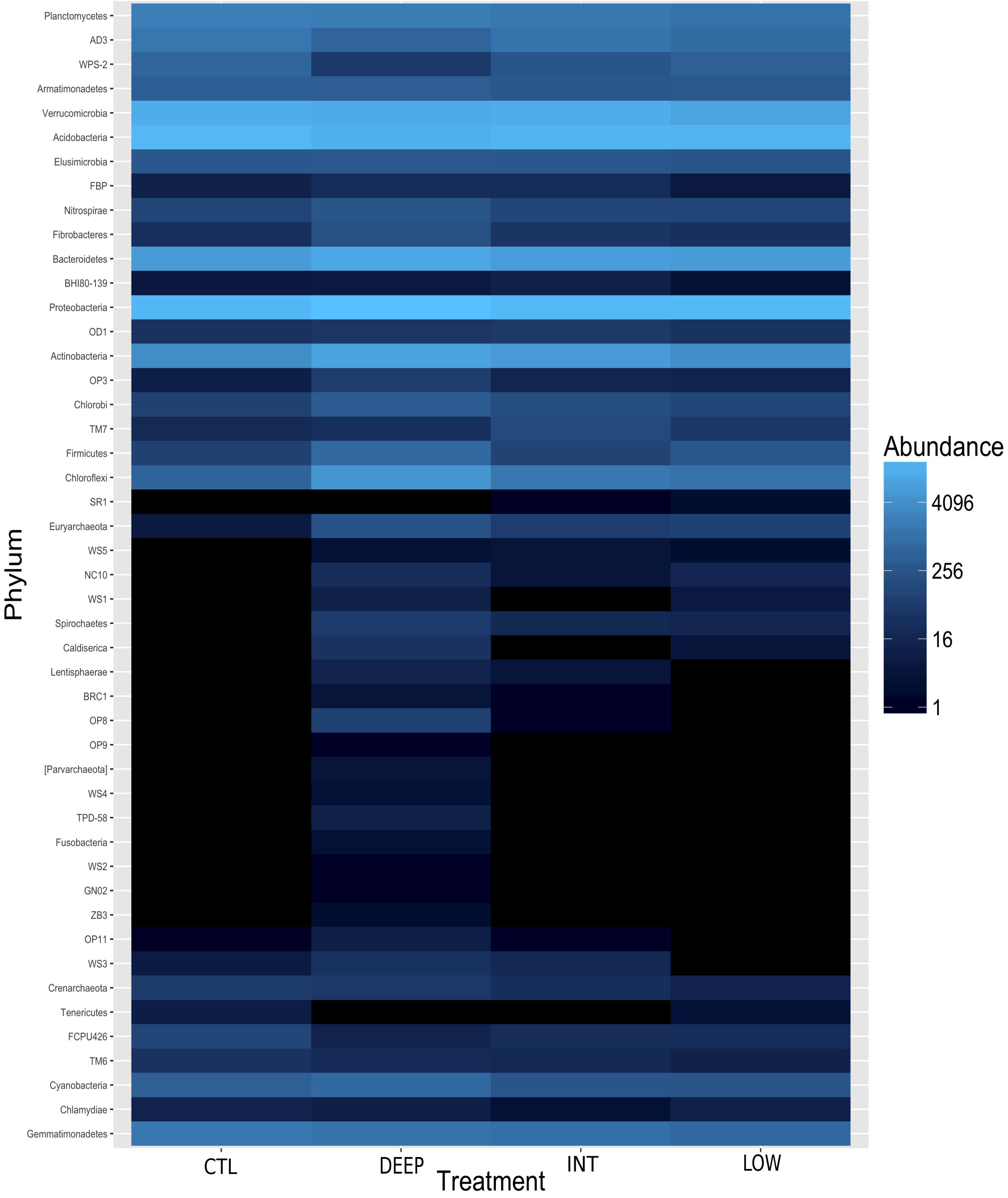

Fig. S16 – Heatmap of raw gene abundance (# of OTU's) for all detected Phyla. Columns represent snow accumulation treatment groups.

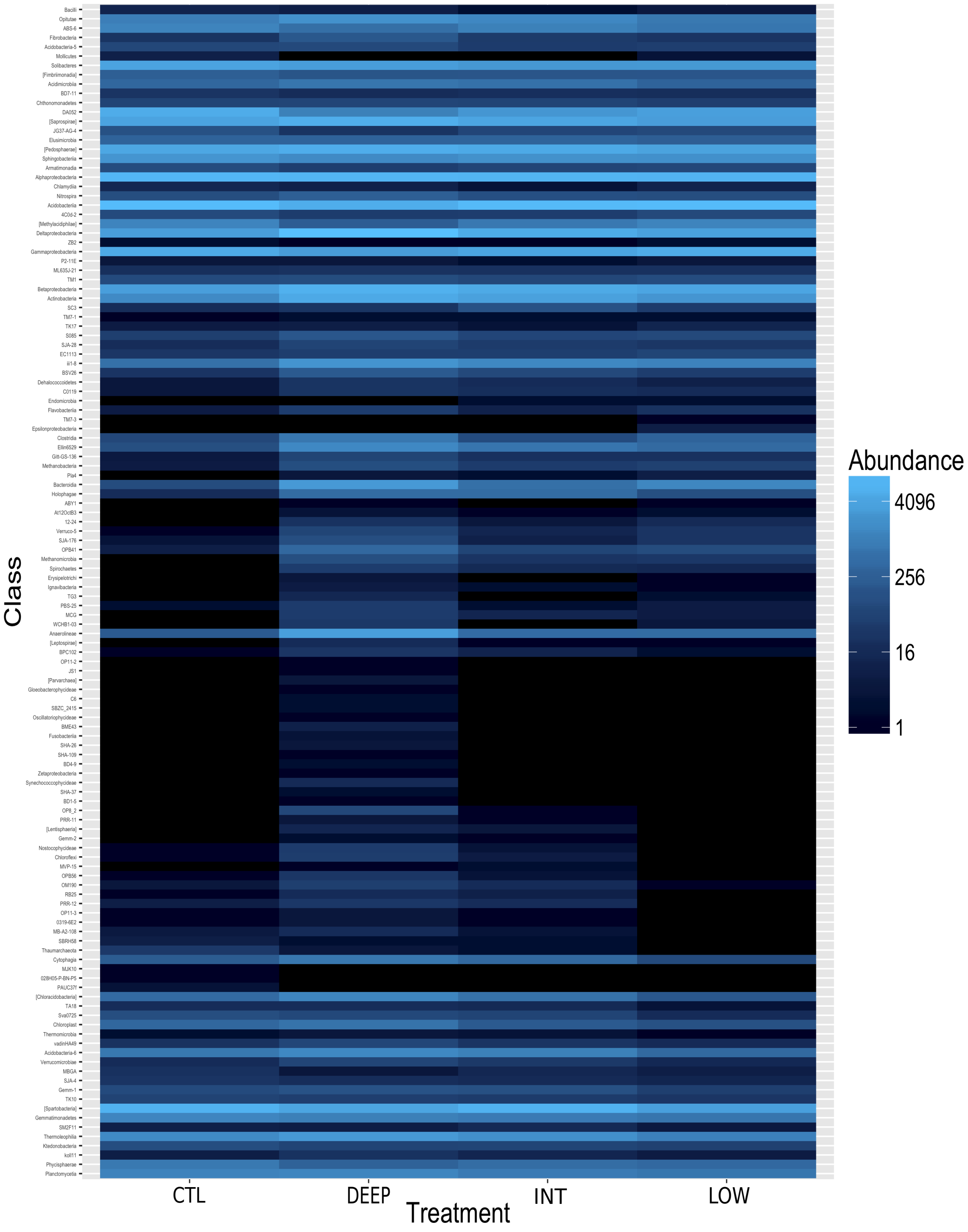

Fig. S17 - Heatmap of raw gene abundance (# of OTU's) for all detected Classes. Columns represent snow accumulation treatment groups.

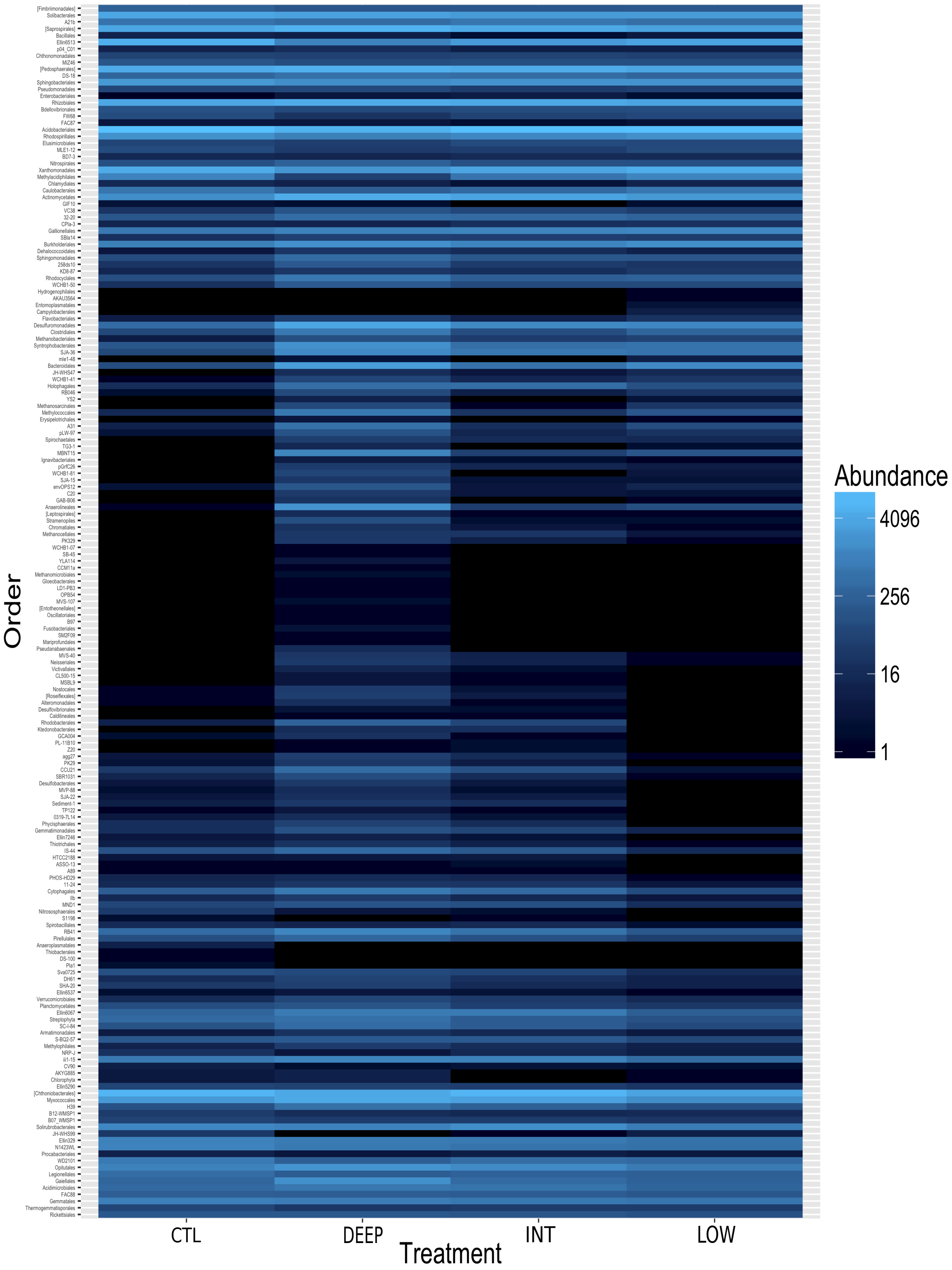

Fig. S18 - Heatmap of raw gene abundance (# of OTU's) for all detected Orders. Columns represent snow accumulation treatment groups.

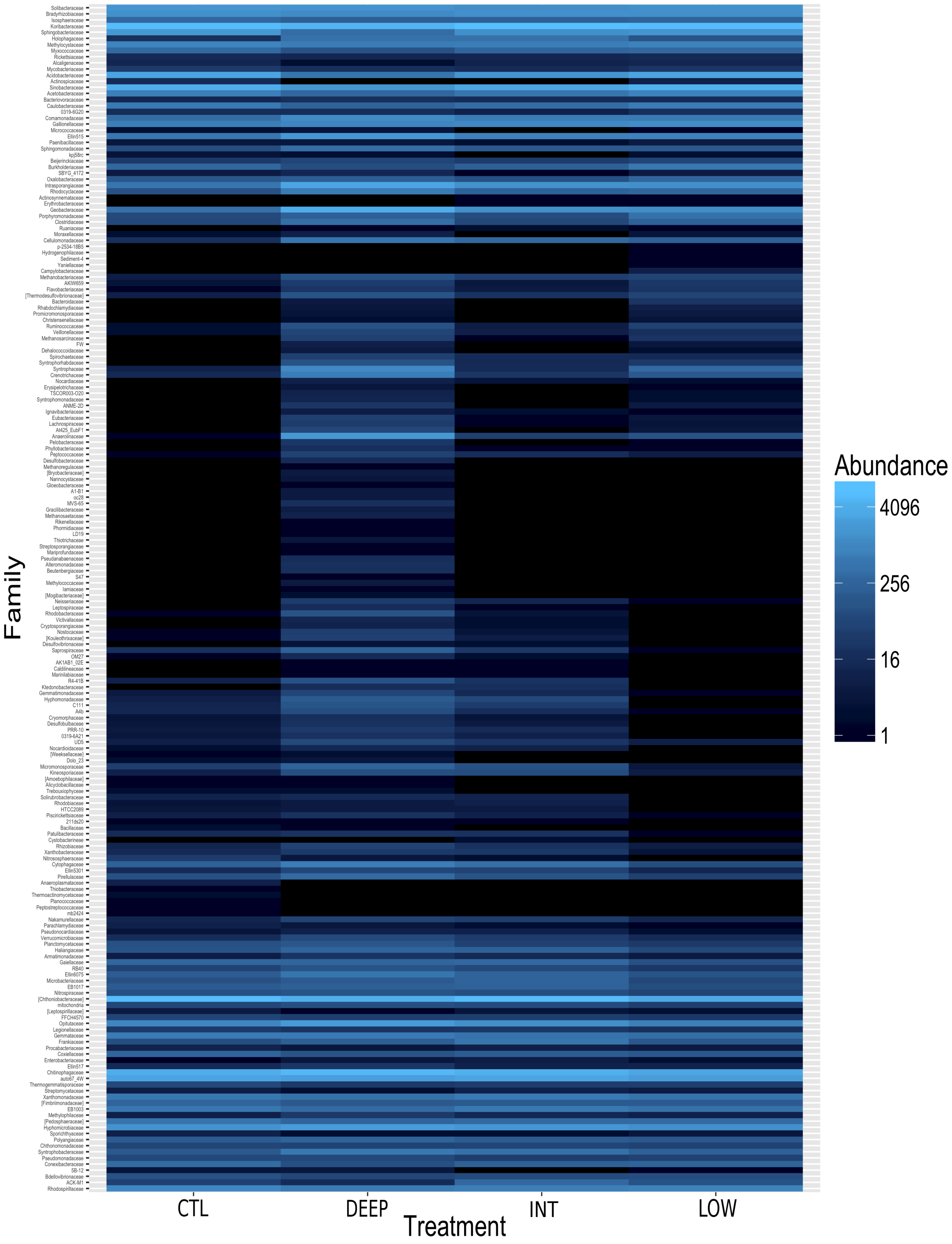

Fig. S19 - Heatmap of raw gene abundance (# of OTU's) for all detected Families. Columns represent snow accumulation treatment groups.

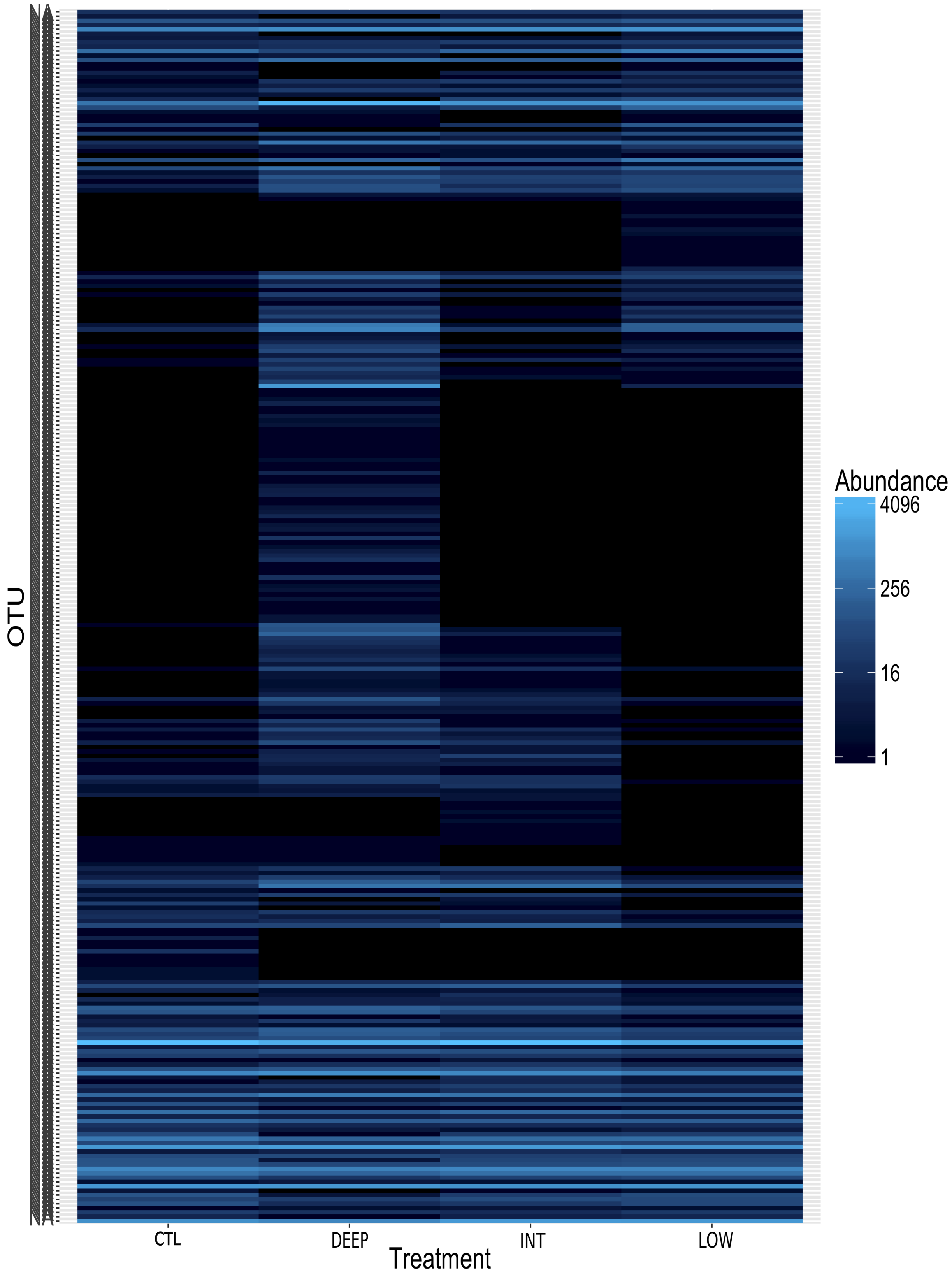

Fig. S20 - Heatmap of raw gene abundance (# of OTU's) for individual OTU assignments. Columns represent snow accumulation treatment groups.